

# GPU-Accelerated OptiX Ray Tracing for Scientific Visualization

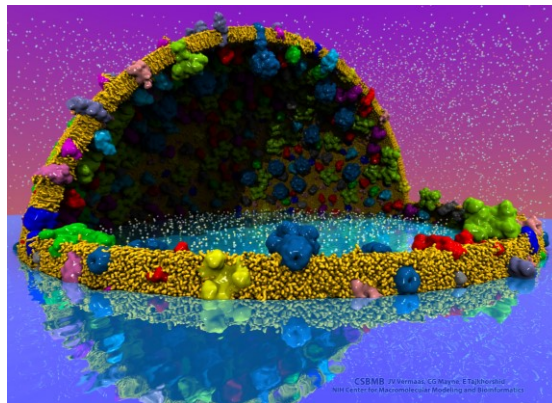
John E. Stone

Theoretical and Computational Biophysics Group  
Beckman Institute for Advanced Science and Technology  
University of Illinois at Urbana-Champaign  
<http://www.ks.uiuc.edu/Research/gpu/>

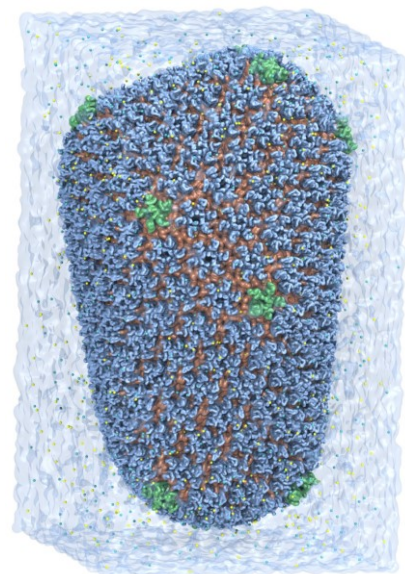
10:00-10:25, NVIDIA Theater, Siggraph 2018  
Vancouver BC, Canada, Thursday August 16<sup>th</sup>, 2018

# VMD – “Visual Molecular Dynamics”

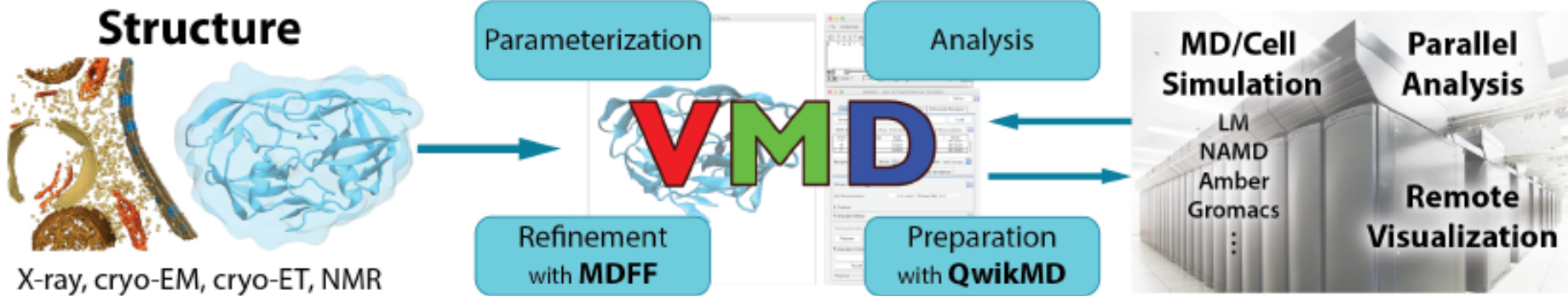
- Visualization and analysis of:
  - Molecular dynamics simulations
  - Lattice cell simulations
  - Quantum chemistry calculations
  - Cryo-EM densities, volumetric data
  - Sequence information
- User extensible scripting and plugins
- <http://www.ks.uiuc.edu/Research/vmd/>



Cell-Scale Modeling



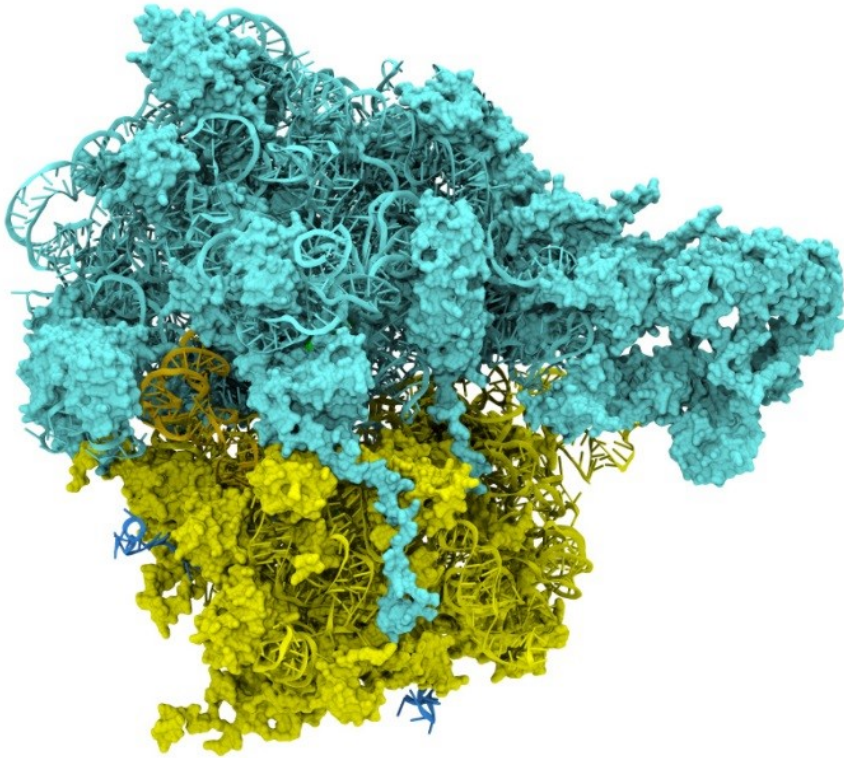
MD Simulation



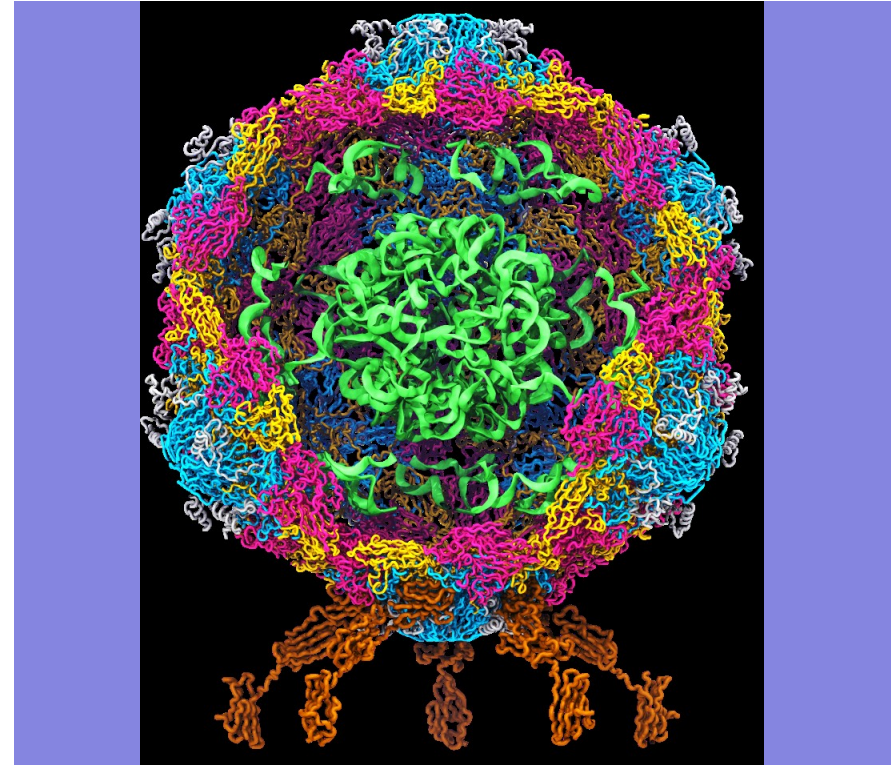
# Goal: A Computational Microscope

Study the molecular machines in living cells

Ribosome: target for antibiotics

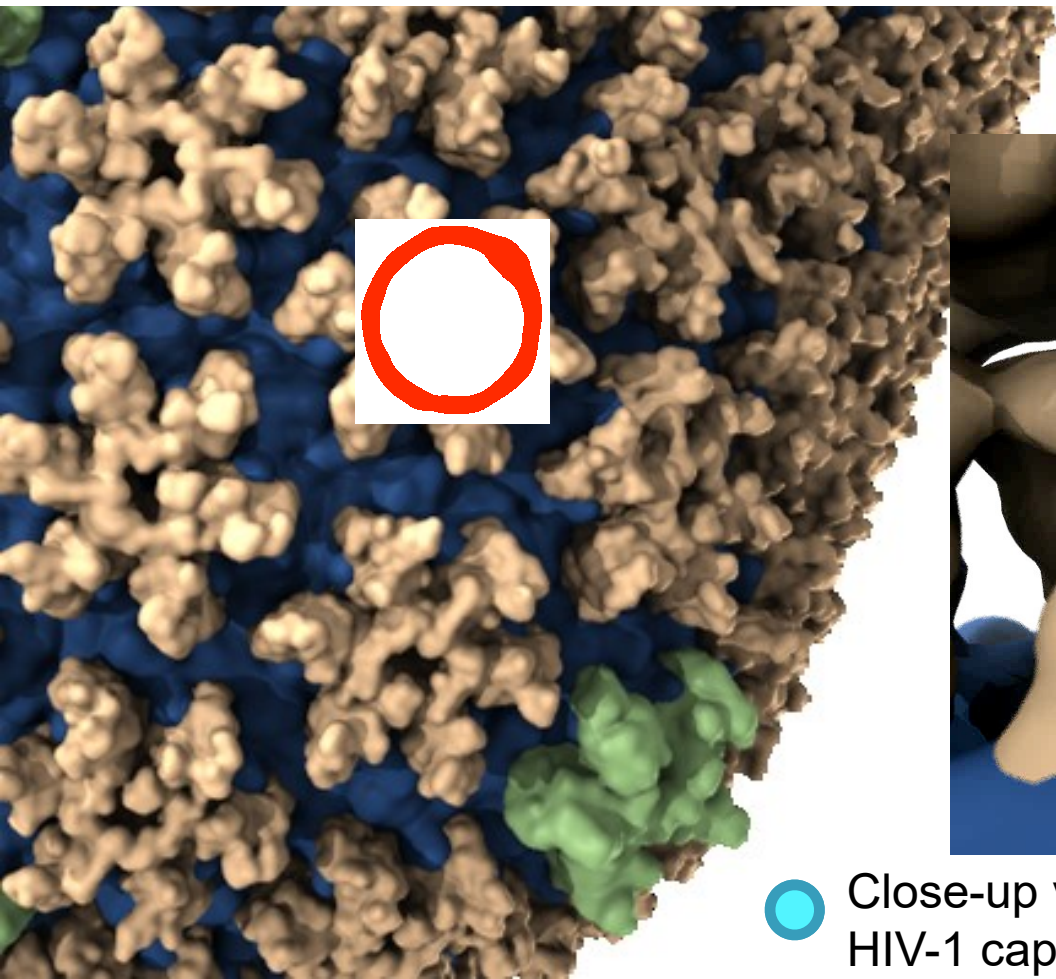


Poliovirus

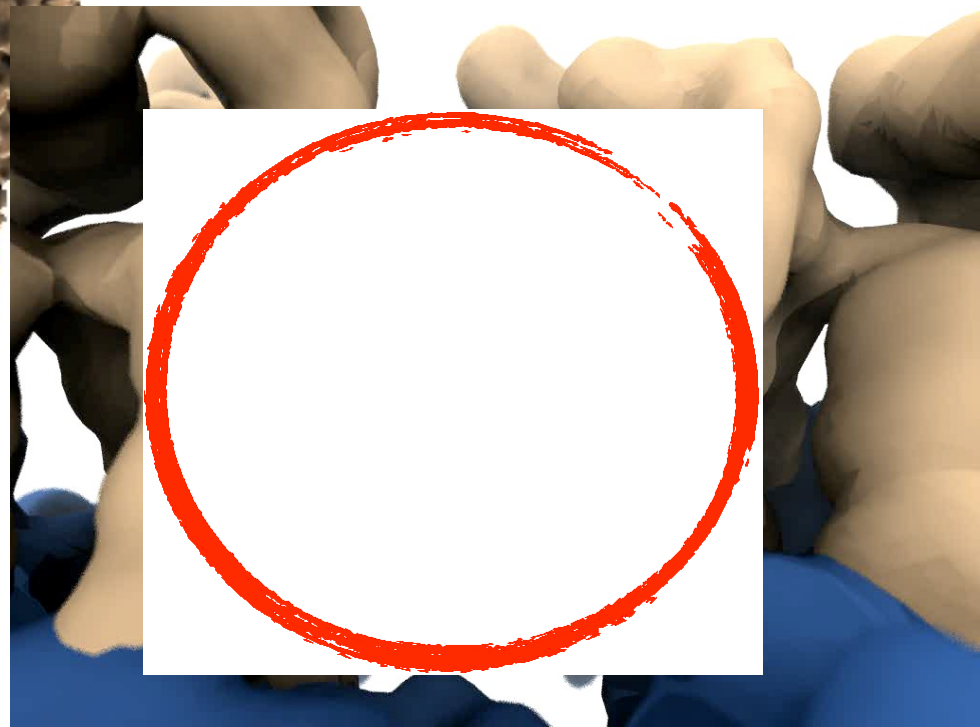




# Goal: Intuitive interactive viz. in crowded molecular complexes



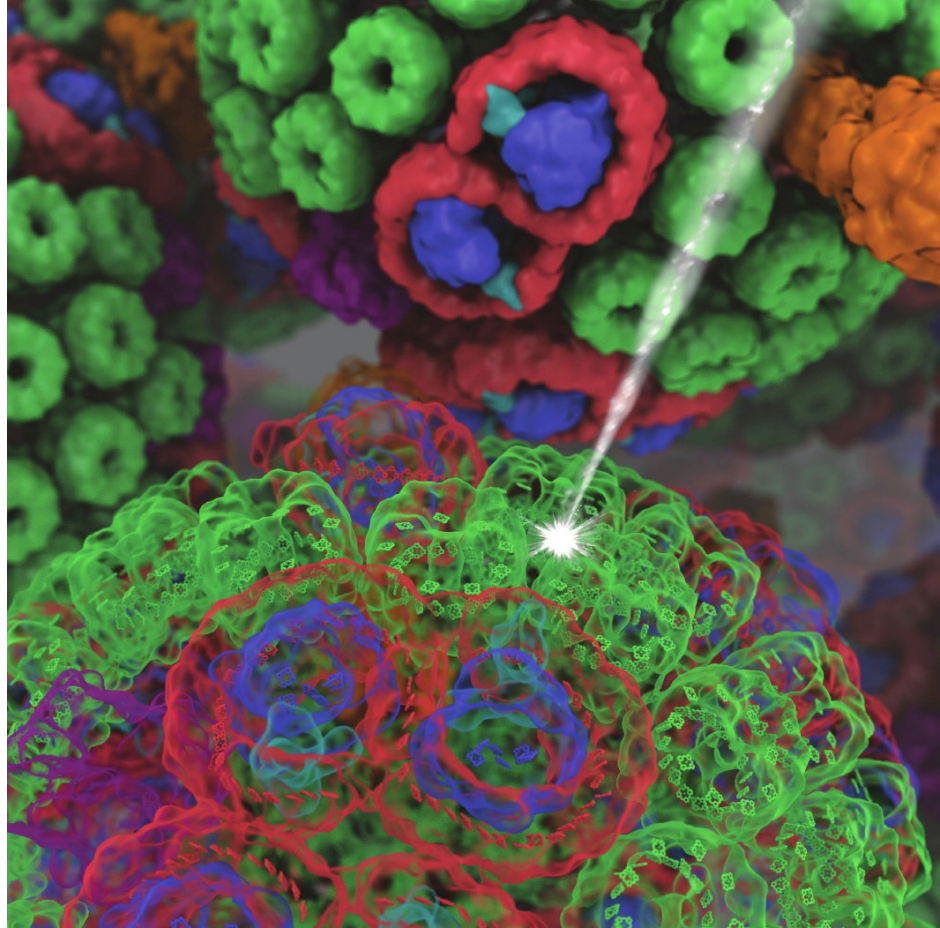
Results from 64M atom, 1  $\mu$ s sim!



Close-up view of chloride ions permeating through HIV-1 capsid hexameric centers

# High Fidelity Ray Tracing with OptiX

- Advanced rendering techniques save scientists time, produce images that are easier to interpret
- Ambient Occlusion, Depth of Field, high quality transparency, instancing, ....
- **Interactive RT** on laptop, desk, cloud
- Interactivity is critically important for scientists that need to obtain results without becoming a graphics expert
- Large-scale parallel rendering:  
in situ or post hoc visualization tasks
- **Stereoscopic panorama and full-dome projections**
- **Omnidirectional VR: YouTube, HMDs**



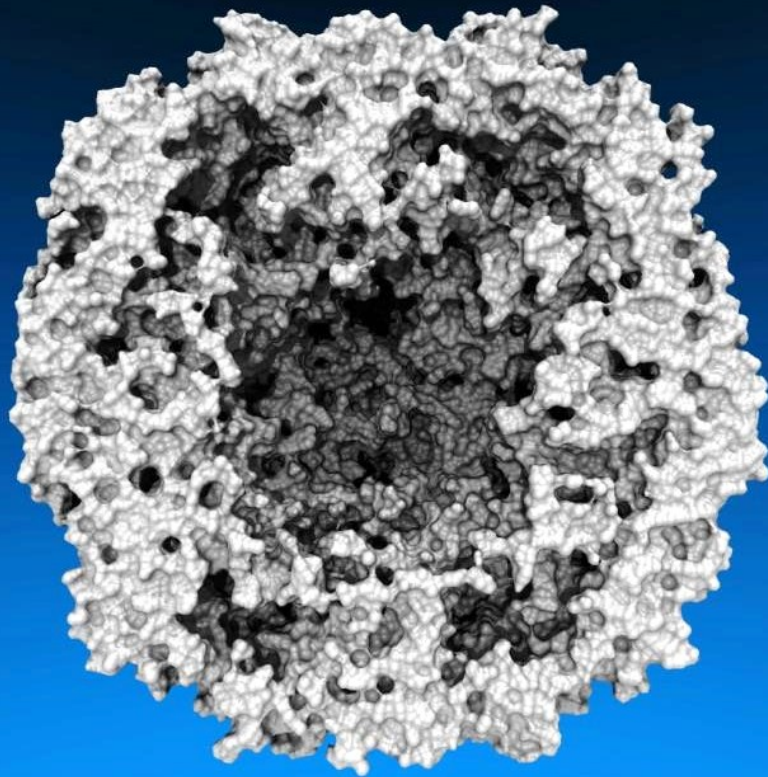
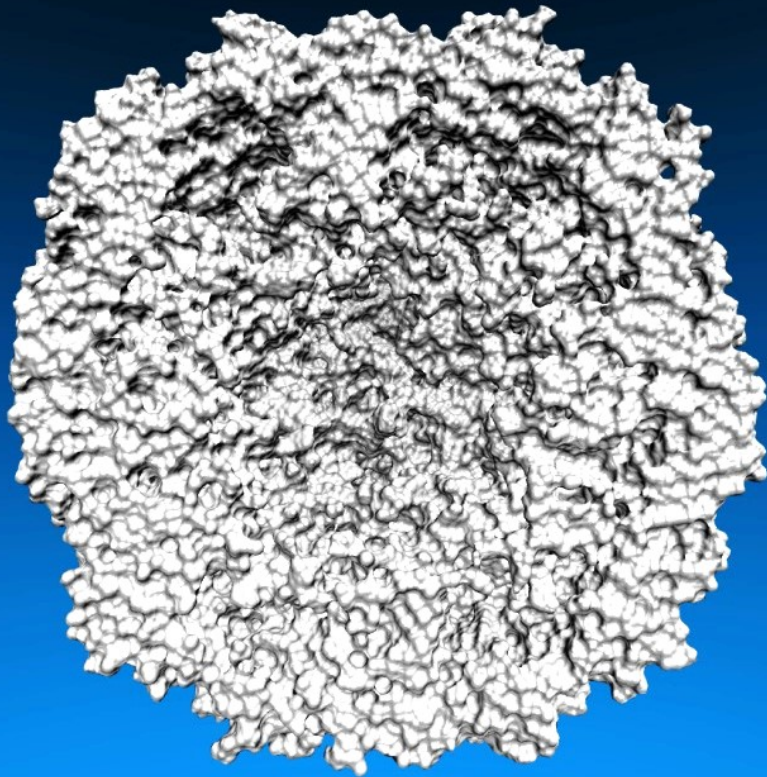
VMD/OptiX all-atom Chromatophore



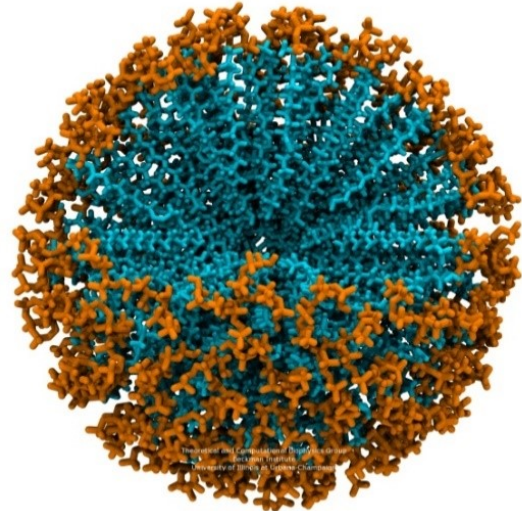
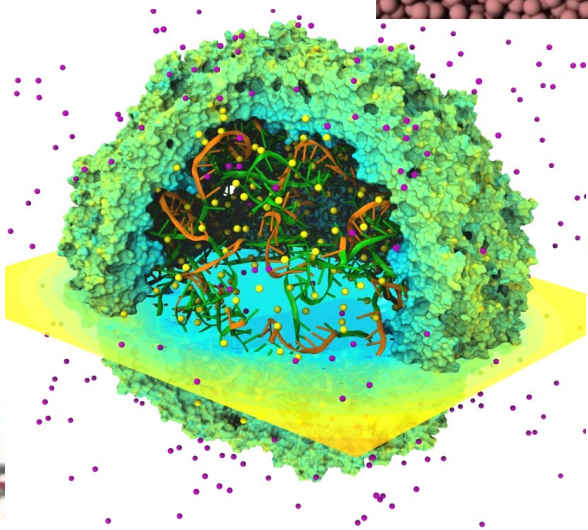
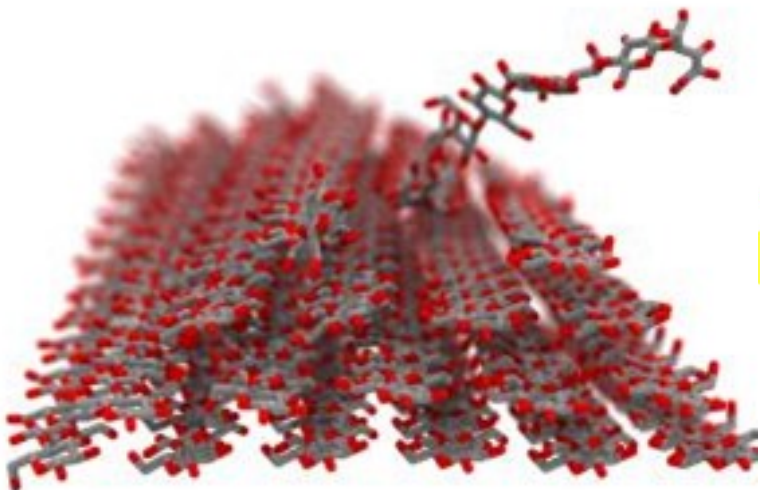
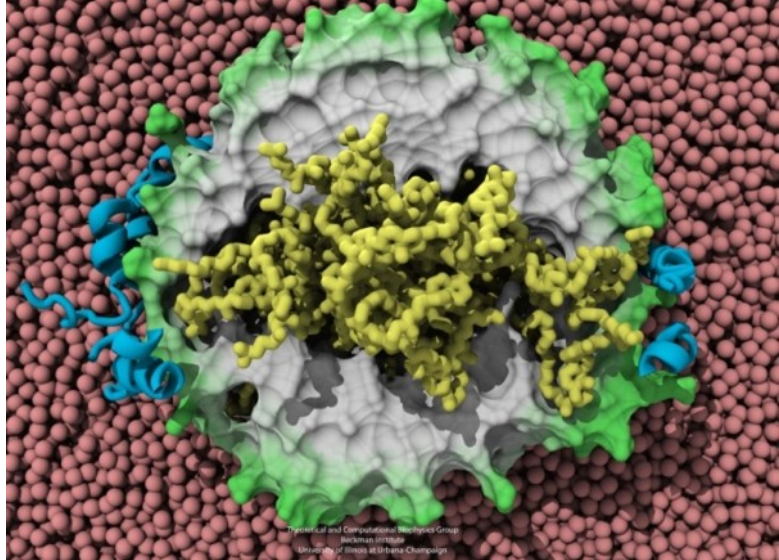
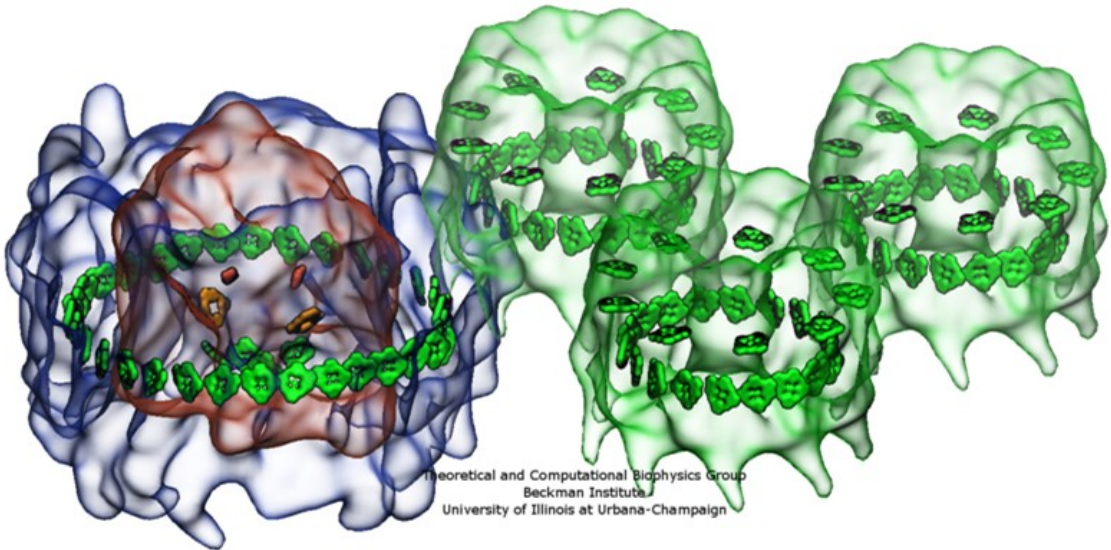
# Lighting Comparison, STMV Capsid

**Two lights, no shadows**

**Ambient occlusion + two lights, 144 AO rays/hit**

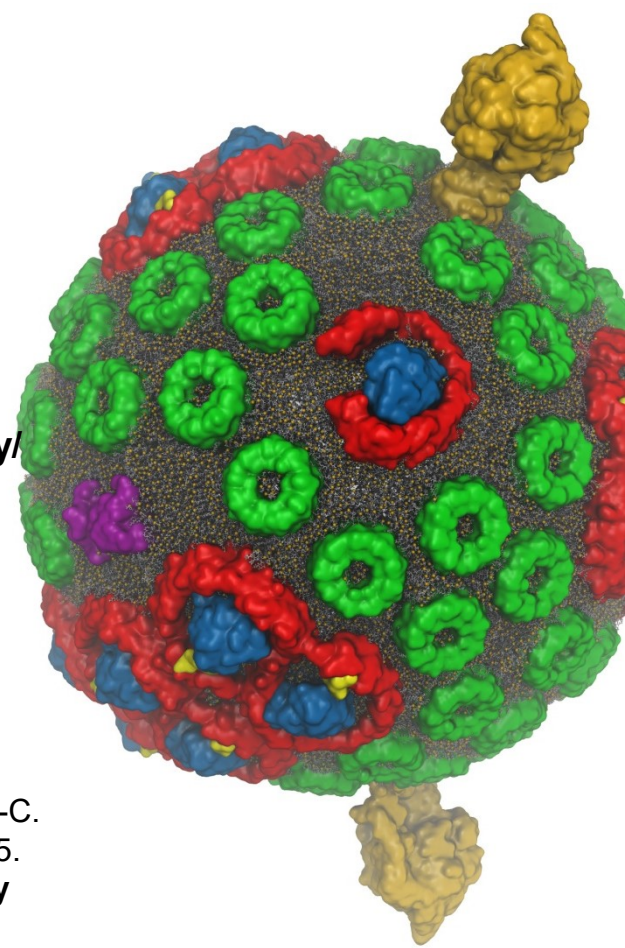






# VMD w/ OptiX

- Interactive RT on laptops, desktops, and cloud
- Large-scale parallel rendering: in situ or post hoc visualization
- Remote RT on NVIDIA GPU clusters
- Stereoscopic panoramic and full-dome projections
- Omnidirectional VR for YouTube, VR HMDs
- **GPU memory sharing via NVLink on Quadro, Tesla GPUs**
- **VMD+OptiX 5, NVIDIA NGC container: <https://ngc.nvidia.com/registry/>**
- **In-progress:**
  - **OptiX denoising support: fast turnaround w/ AO, DoF, etc**



## **GPU-Accelerated Molecular Visualization on Petascale Supercomputing Platforms.**

J. E. Stone, K. L. Vandivort, and K. Schulten. UltraVis'13, pp. 6:1-6:8, 2013.

## **Visualization of Energy Conversion Processes in a Light Harvesting Organelle at Atomic Detail.**

M. Sener, et al. SC'14 Visualization and Data Analytics Showcase, 2014.

## **Chemical Visualization of Human Pathogens: the Retroviral Capsids.**

J. R. Perilla, B.-C. Goh, J. E. Stone, and K. Schulten. SC'15 Visualization and Data Analytics Showcase, 2015.

## **Atomic Detail Visualization of Photosynthetic Membranes with GPU-Accelerated Ray Tracing.**

J. E. Stone et al., J. Parallel Computing, 55:17-27, 2016.

## **Immersive Molecular Visualization with Omnidirectional Stereoscopic Ray Tracing and Remote Rendering**

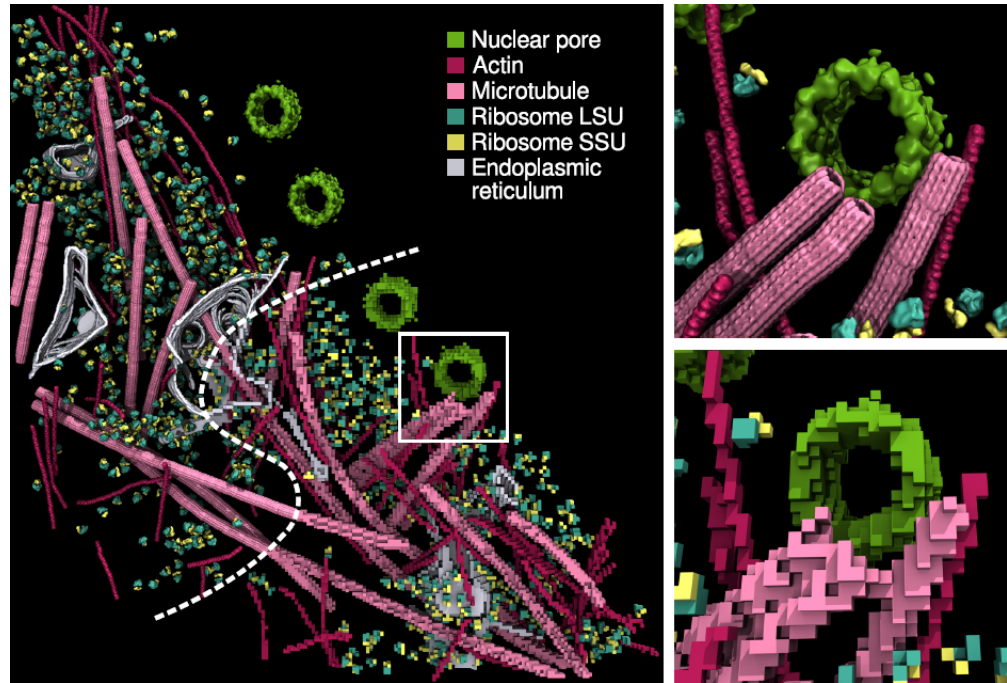
J. E. Stone, W. R. Sherman, and K. HPDAV, IPDPSW, pp. 1048-1057, 2016.

**VMD/OptiX GPU Ray Tracing of all-atom Chromatophore w/ lipids.**



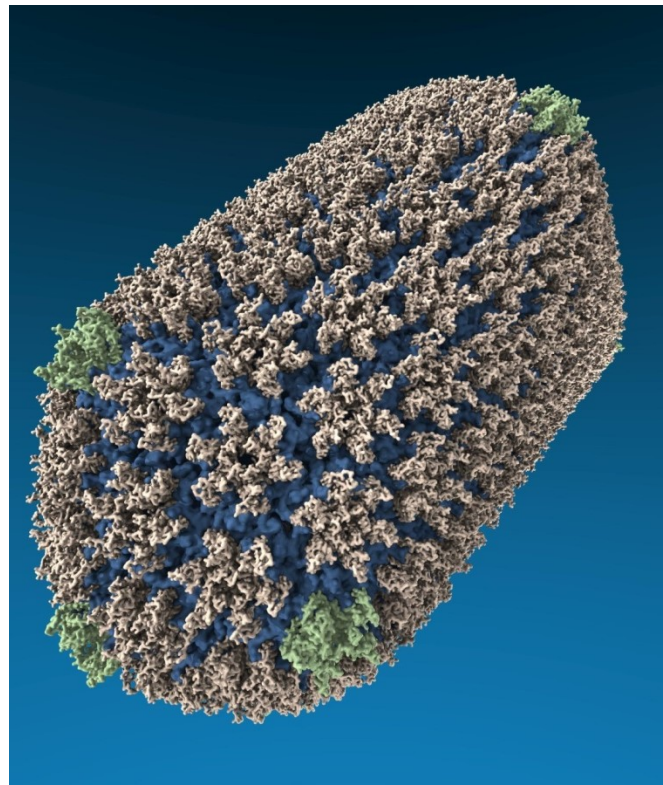
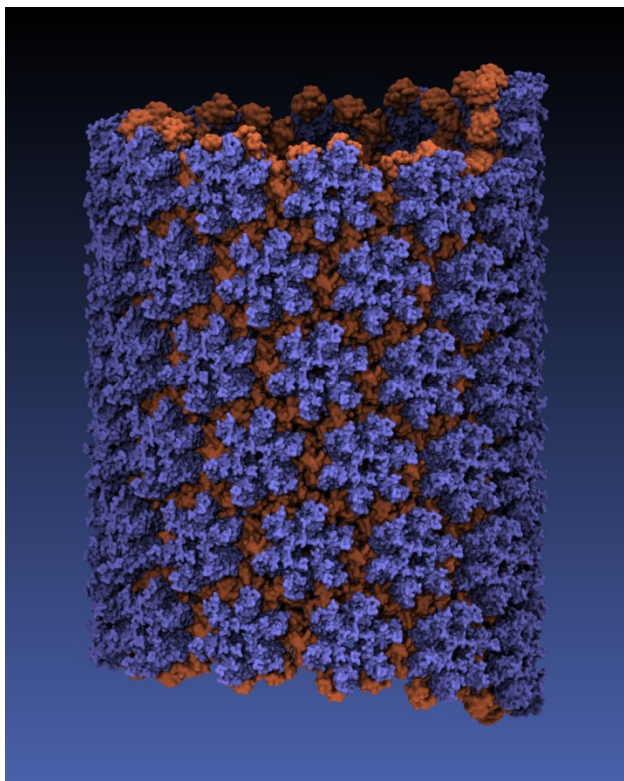
# Interactive Ray Tracing of Cells

- High resolution cellular tomograms, **billions of voxels**
- Even isosurface or lattice site graphical representations involve ~100M geometric primitives
- 24GB GPUs allow interactive RT of large cellular tomograms
- **VMD exploits GPUs with NVLink and OptiX distribution of scene data across multiple GPUs for greater capacity and higher performance**



Earnest, et al. J. Physical Chemistry B, 121(15): 3871-3881, 2017.

# VMD “QuickSurf” Representation, Ray Tracing

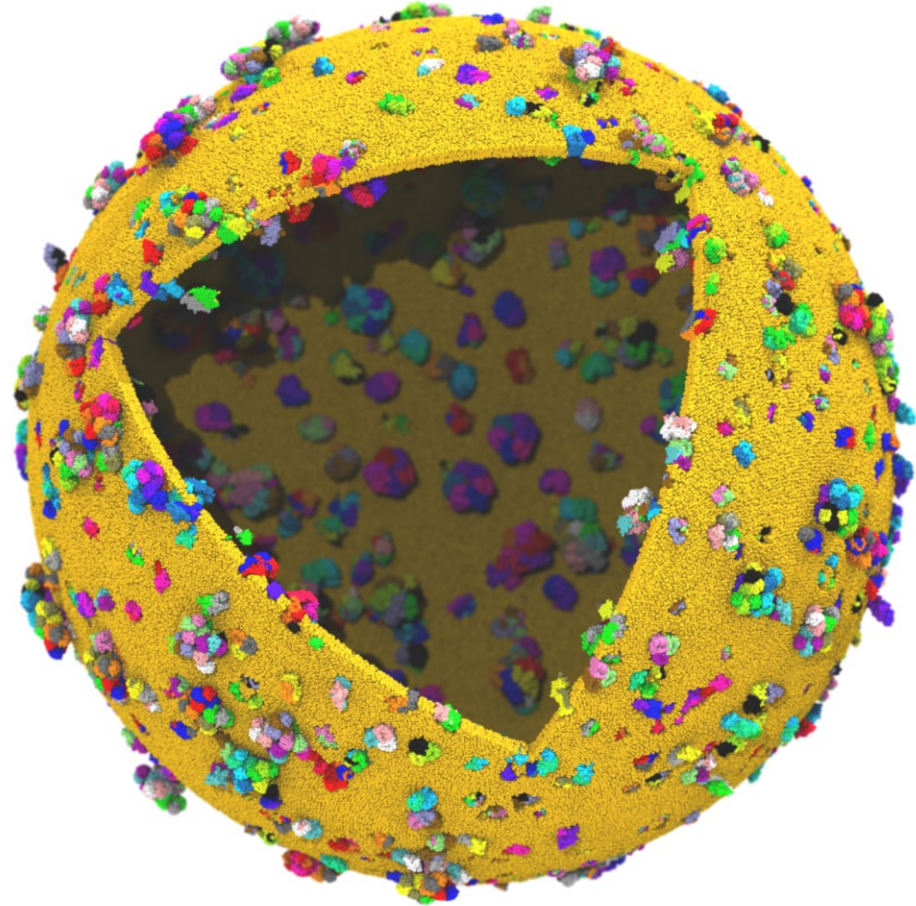


**All-atom HIV capsid simulations w/ up to 64M atoms on Blue Waters**



# Next Generation: Simulating a Proto-Cell

- **ORNL Summit:  
NVLink-connected Tesla V100  
GPUs enable next-gen  
visualizations**
- 200nm diameter
- ~1 billion atoms w/ solvent
- ~1400 proteins in membrane

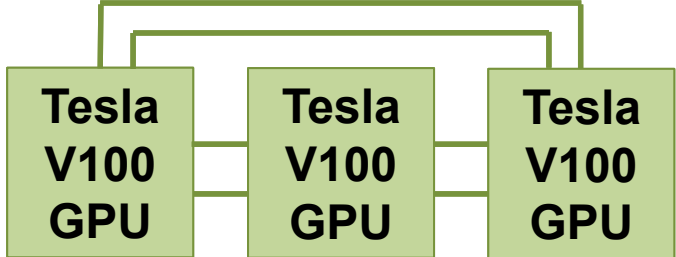


# IBM AC922, ORNL Summit Node

3 GPUs Per CPU Socket

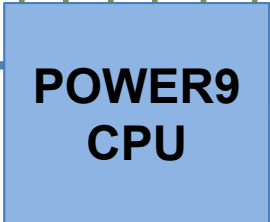


Nvlink 2.0  
2x 50GBps:  
**100GBps**

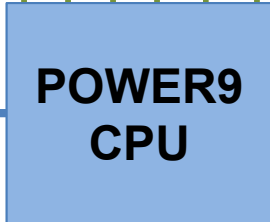


DDR4  
DRAM

120GBps



X-Bus  
64GBps



120GBps

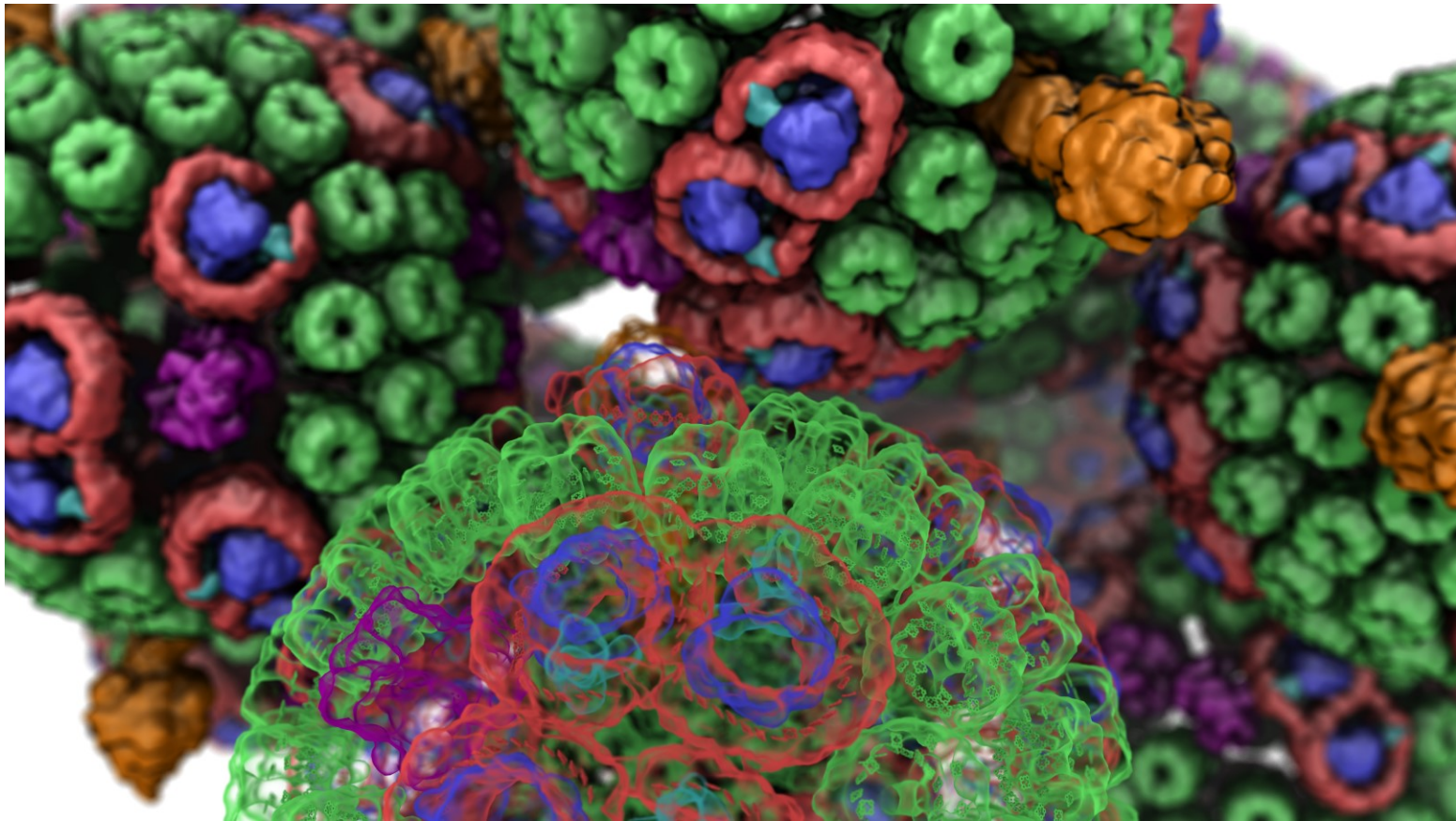
DDR4  
DRAM

InfiniBand  
12GBps

InfiniBand  
12GBps

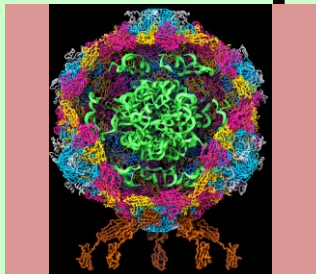


# VMD/OpiX RTX Acceleration



# VMD Molecular Structure Data and Global State

## Scene Graph



## Graphical Representations

DrawMolecule

Non-Molecular  
Geometry

## User Interface Subsystem

Tcl/Python Scripting

Mouse + Windows

VR Input "Tools"

## Display Subsystem

VMDDisplayList

DisplayDevice

OpenGLDisplayDevice

FileRenderer

Windowed OpenGL GPU

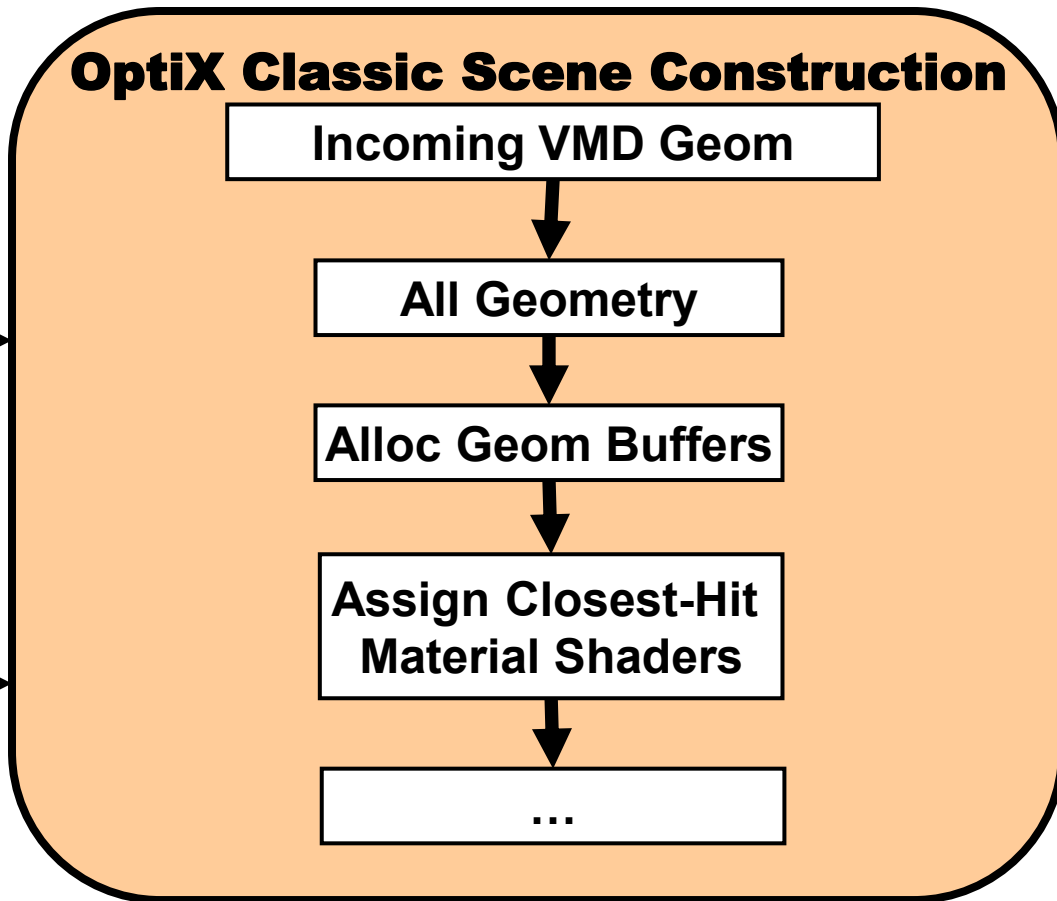
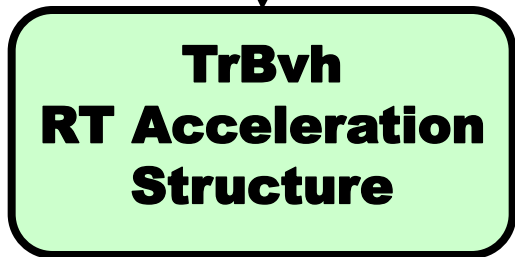
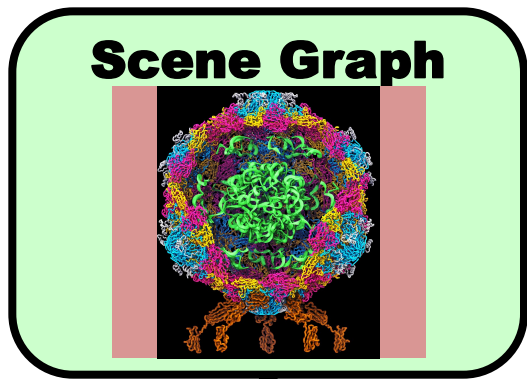
OpenGL Pbuffer GPU

Tachyon CPU RT

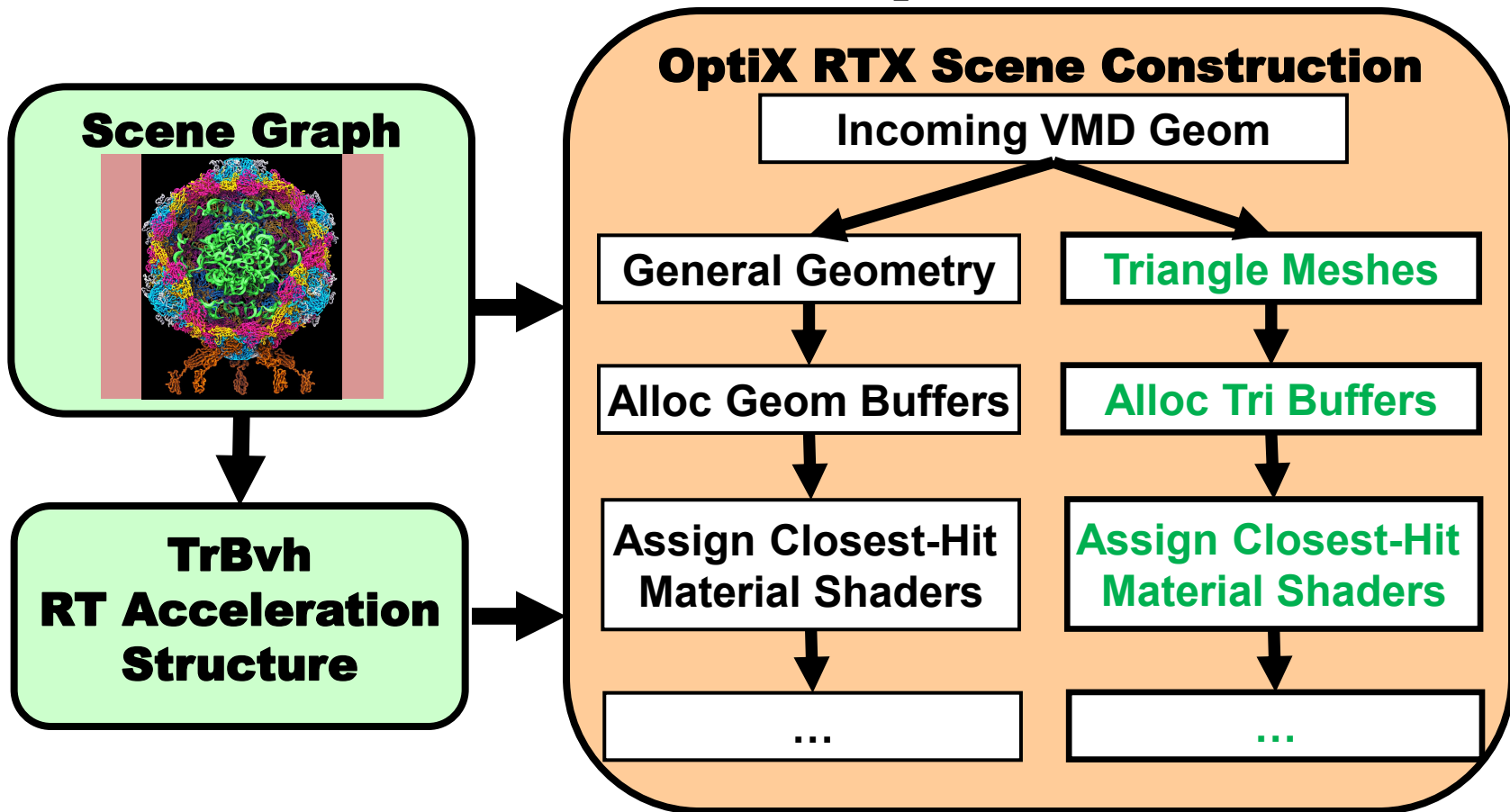
TachyonL-OptiX GPU RT  
Batch + Interactive



# VMD Scene w/ OptiX Classic APIs

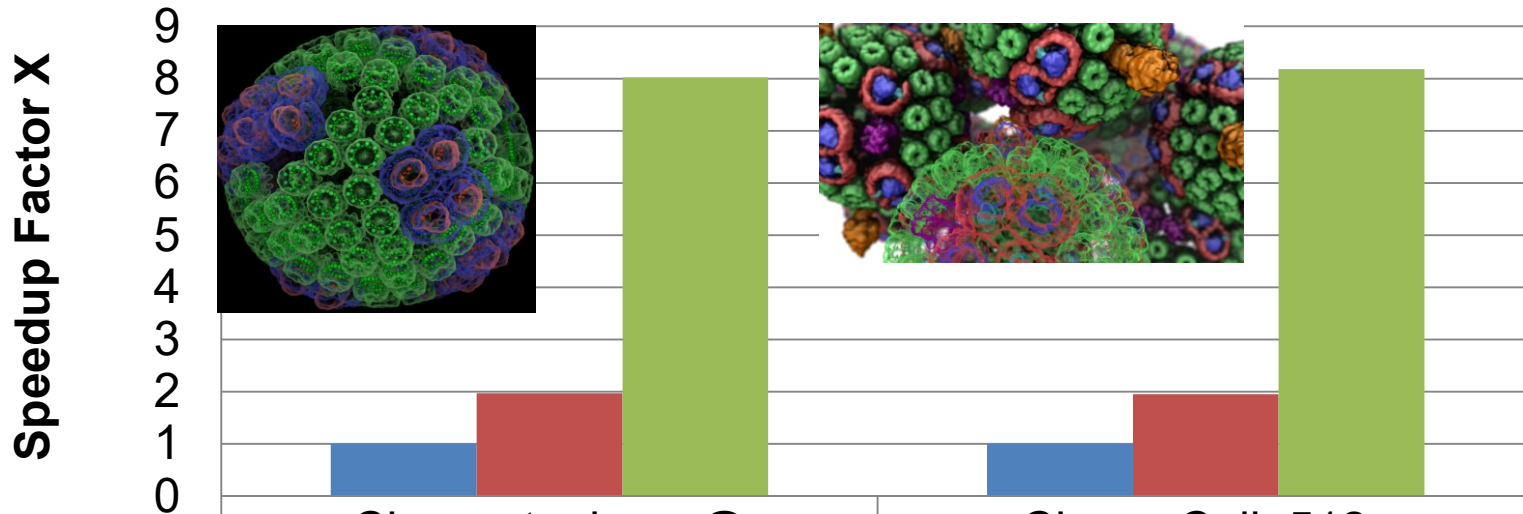


# VMD Scene w/ OptiX RTX APIs





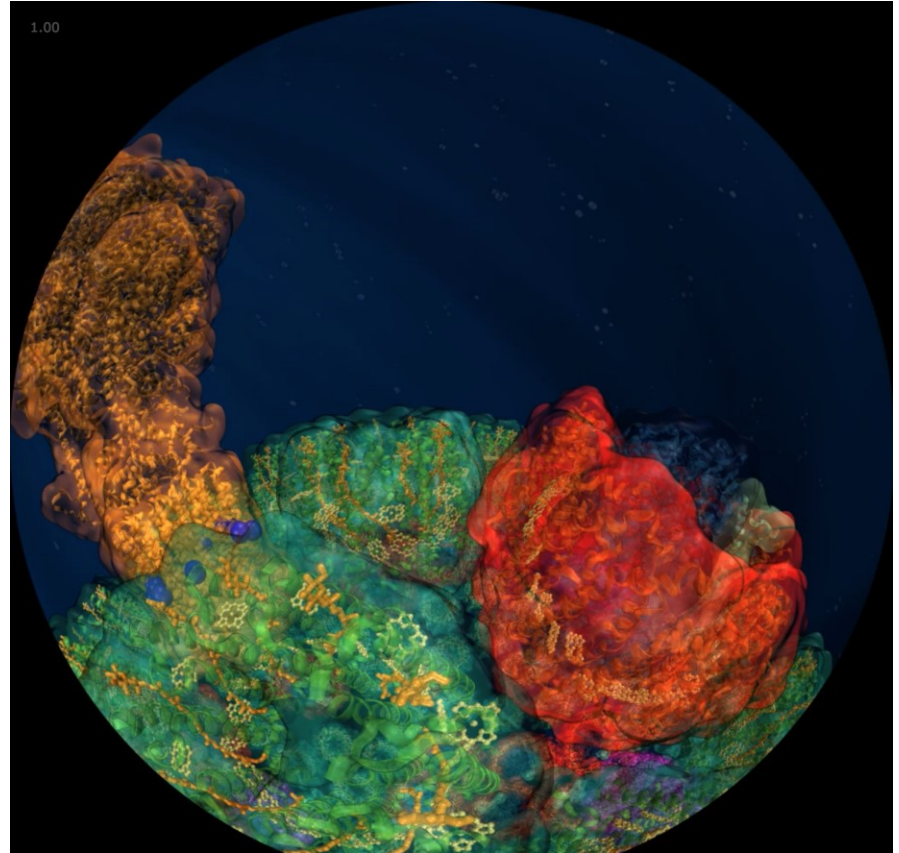
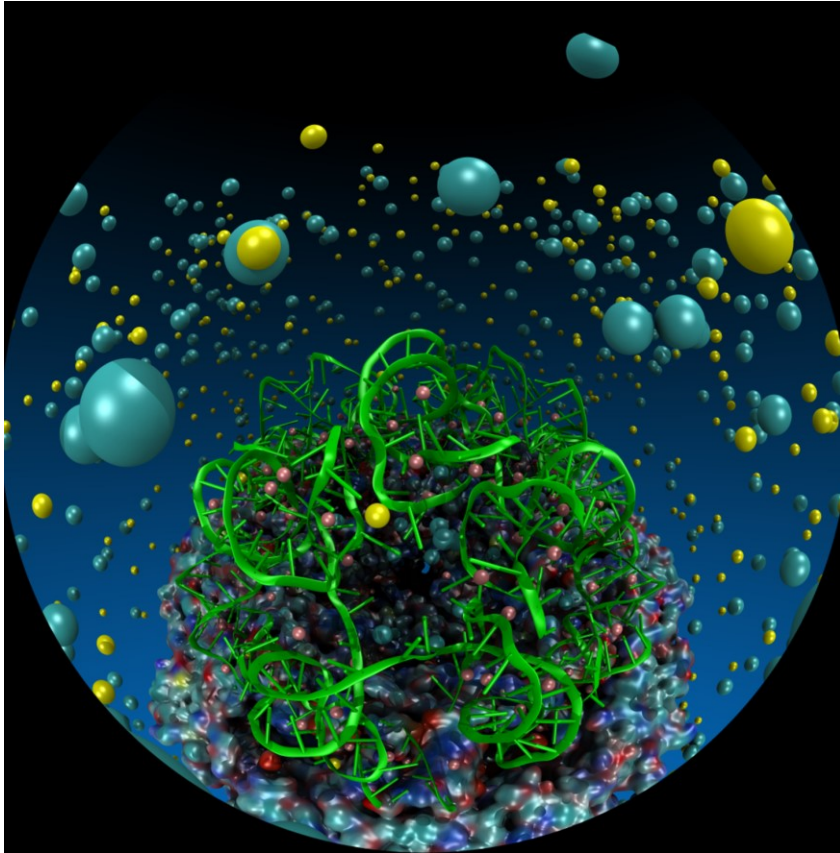
# VMD OptiX RT performance on Quadro RTX 6000



	Chromatophore @ 4Kx4K	Chrom Cell, 512x DoF @ 1080p
■ Quadro GV100	1	1
■ 2x Quadro GV100	1.97	1.95
■ Quadro RTX 6000	8.02	8.18

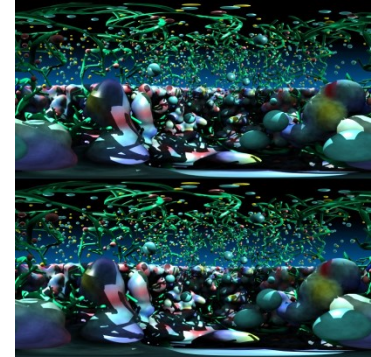
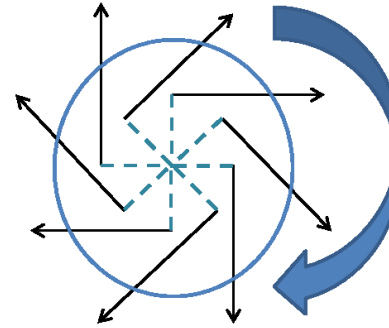
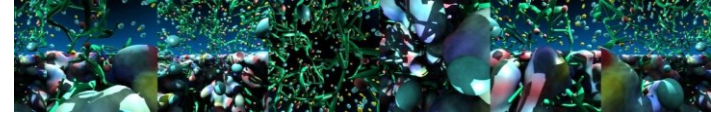
# Planetarium Dome Master Projections

NSF CADENS Dome Show w/ NCSA AVL



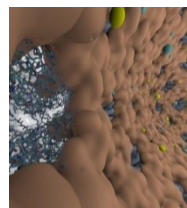
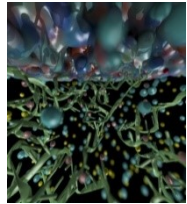
# Omnidirectional Stereoscopic Ray Tracing

- Ray trace 360° images and movies for Desk and VR HMDs: Oculus, Vive, Cardboard
- Stereo spheremaps or cubemaps allow very high-frame-rate interactive OpenGL display
- **AO lighting, depth of field, shadows, transparency, curved geometry, ...**

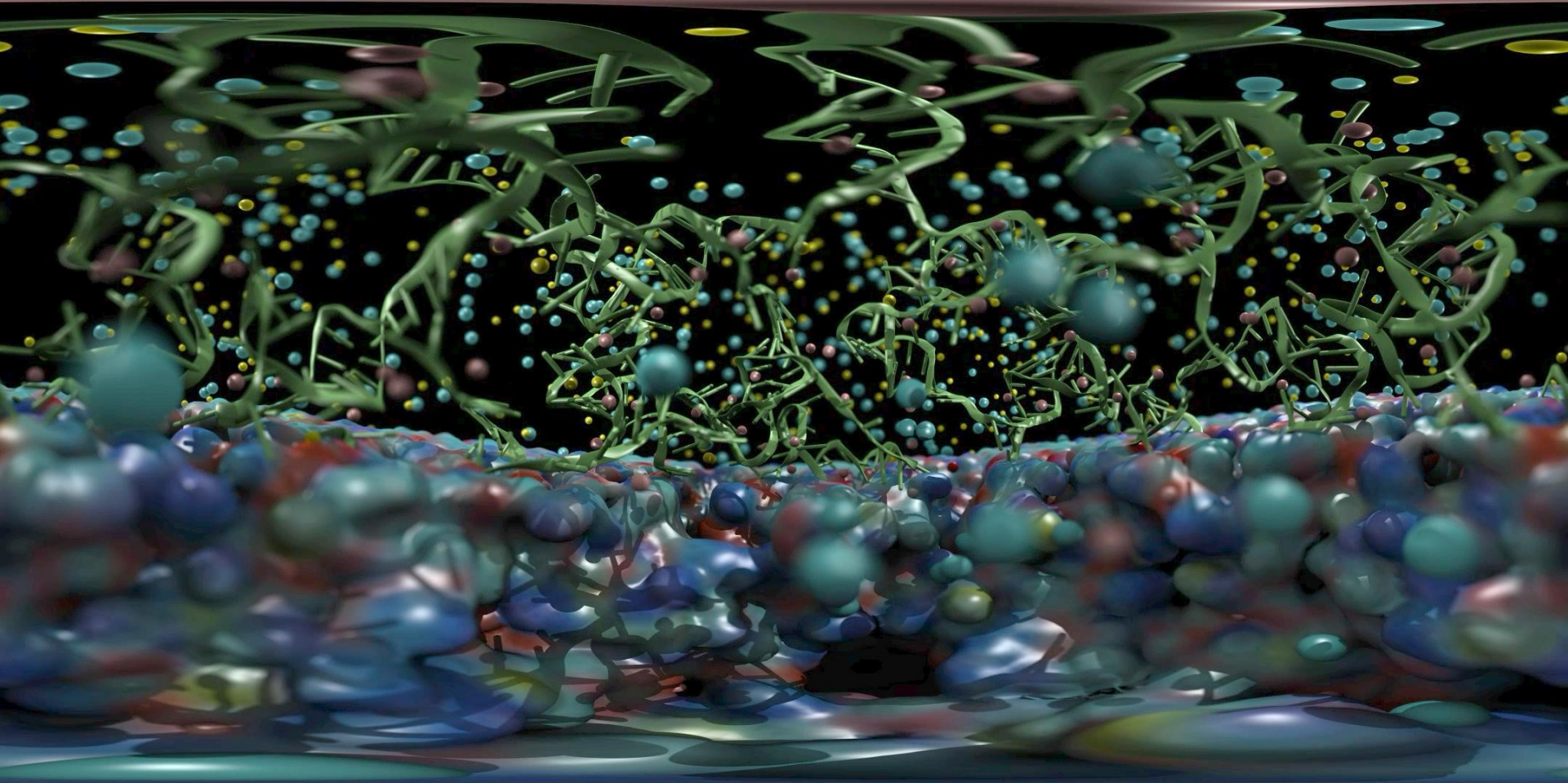


**Atomic Detail Visualization of Photosynthetic Membranes with GPU-Accelerated Ray Tracing.** J. E. Stone, et al. J. Parallel Computing, 55:17-27, 2016.

**Immersive Molecular Visualization with Omnidirectional Stereoscopic Ray Tracing and Remote Rendering.** J. E. Stone, W. R. Sherman, and K. Schulten. High Performance Data Analysis and Visualization Workshop, IEEE International Parallel and Distributed Processing Symposium Workshops (IPDPSW), pp. 1048-1057, 2016.

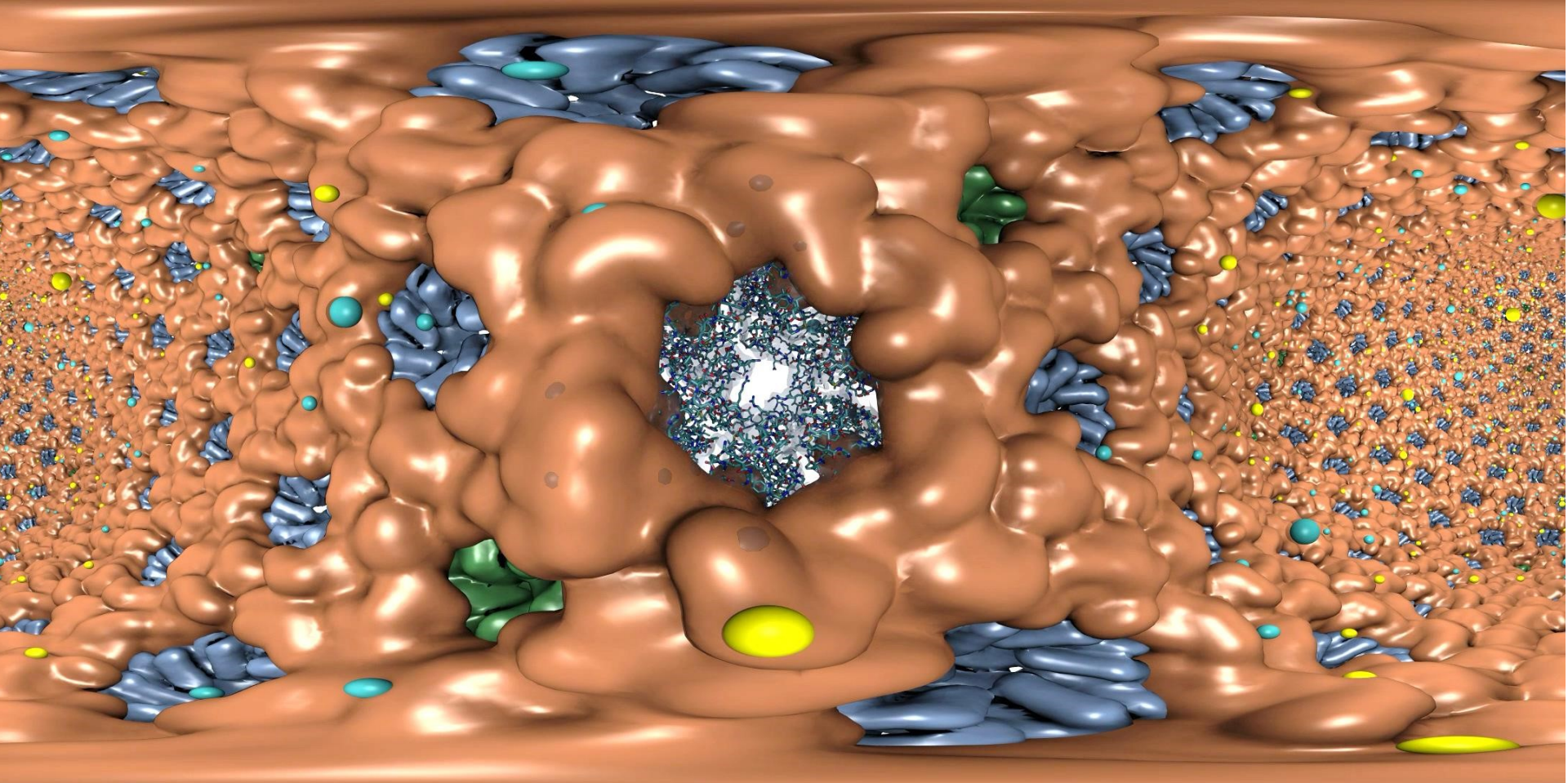




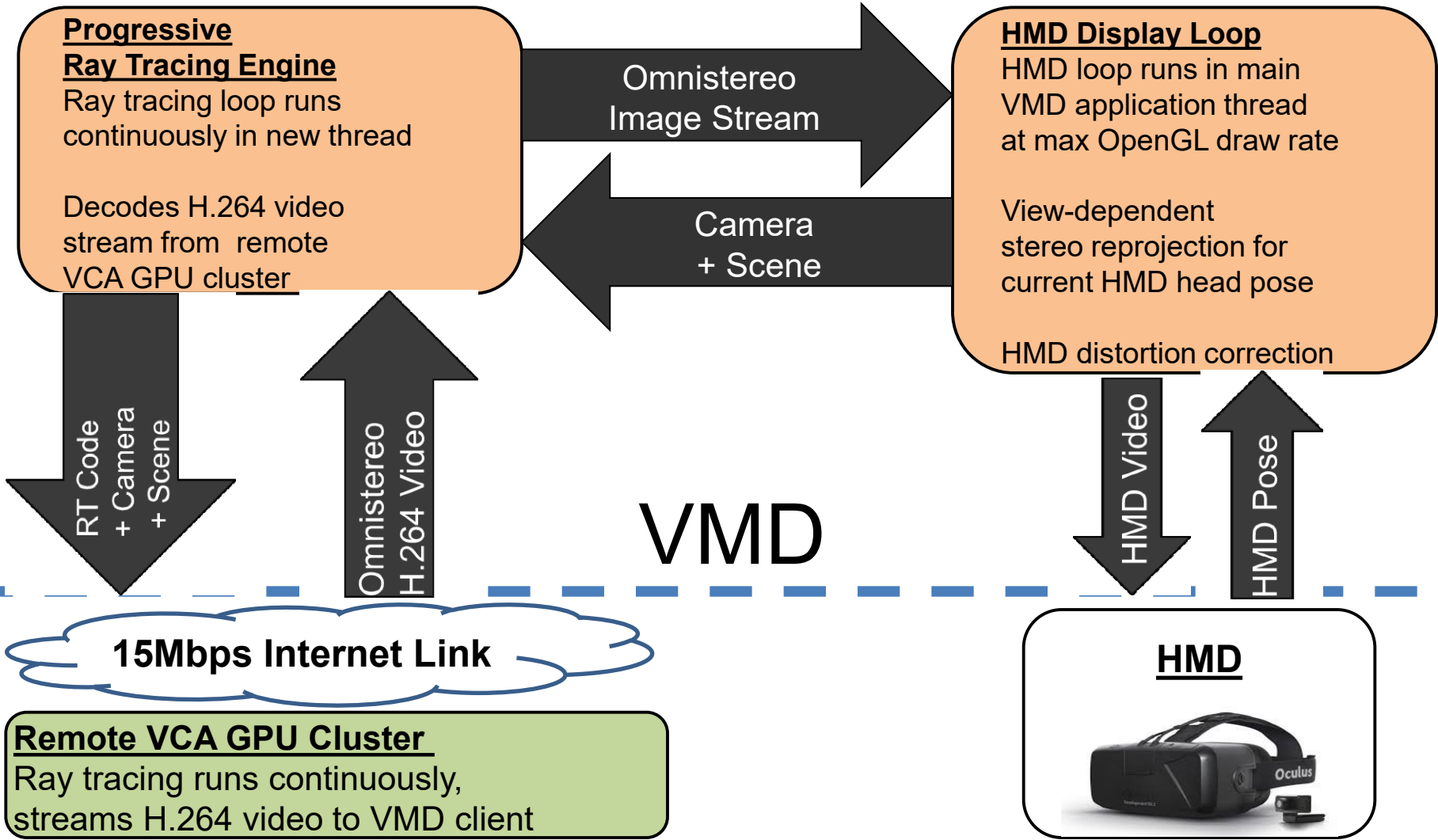


**Satellite Tobacco Mosaic Virus: Capsid, Interior RNA, and Ions  
Ambient Occlusion Lighting, Depth-of-Field Focal Blur, ...**





**HIV-1 Capsid, Capsid Hexamer Detail, and Ions  
Range-Limited Ambient Occlusion Lighting, VR “Headlight”, ...**







**Immersive Molecular Visualization with Omnidirectional Stereoscopic Ray Tracing and Remote Rendering.** J. E. Stone, W. R. Sherman, and K. Schulten. High Performance Data Analysis and Visualization Workshop, IEEE International Parallel and Distributed Processing Symposium Workshops (IPDPSW), pp. 1048-1057, 2016.

# Making Our Research Tools Easily Accessible

- Docker “container” images available in NVIDIA NGC registry
  - Users obtain Docker images via registry, download and run on the laptop, workstation, cloud, or supercomputer of their choosing
  - <https://ngc.nvidia.com/registry/>
  - <https://ngc.nvidia.com/registry/hpc-vmd>
- Cloud based deployment
  - Full virtual machines (known as “AMI” in Amazon terminology)
  - Amazon AWS EC2 GPU-accelerated instances:  
<http://www.ks.uiuc.edu/Research/cloud/>



Clusters, Supercomputers

Workstations,  
Servers,  
Cloud



## **Molecular dynamics-based refinement and validation for sub-5 Å cryo-electron microscopy**

**maps.** Abhishek Singharoy, Ivan Teo, Ryan McGreevy, John E. Stone, Jianhua Zhao, and Klaus Schulten. *eLife*, 10.7554/eLife.16105, 2016. (66 pages).

**QwikMD-integrative molecular dynamics toolkit for novices and experts.** Joao V. Ribeiro, Rafael C. Bernardi, Till Rudack, John E. Stone, James C. Phillips, Peter L. Freddolino, and Klaus Schulten. *Scientific Reports*, 6:26536, 2016.

**High performance molecular visualization: In-situ and parallel rendering with EGL.** John E. Stone, Peter Messmer, Robert Sisneros, and Klaus Schulten. *2016 IEEE International Parallel and Distributed Processing Symposium Workshop (IPDPSW)*, pp. 1014-1023, 2016.



# VMD / NAMD / LM, NGC Containers



### Documentation

How to use NGC containers on supported platforms >

### Repositories

**nvidia** ^

**hpc** v

- candle
- gamess
- gromacs
- lammers
- lattice-microbes
- namd
- relion
- vmd

**nvidia-hpcvis** v

- index
- paraview-holodeck
- paraview-index
- paraview-optim

### hpc/vmd

```
docker pull nvcr.io/hpc/vmd:cuda9-ubuntu1604-egl-1.9.4a17
```



## VMD

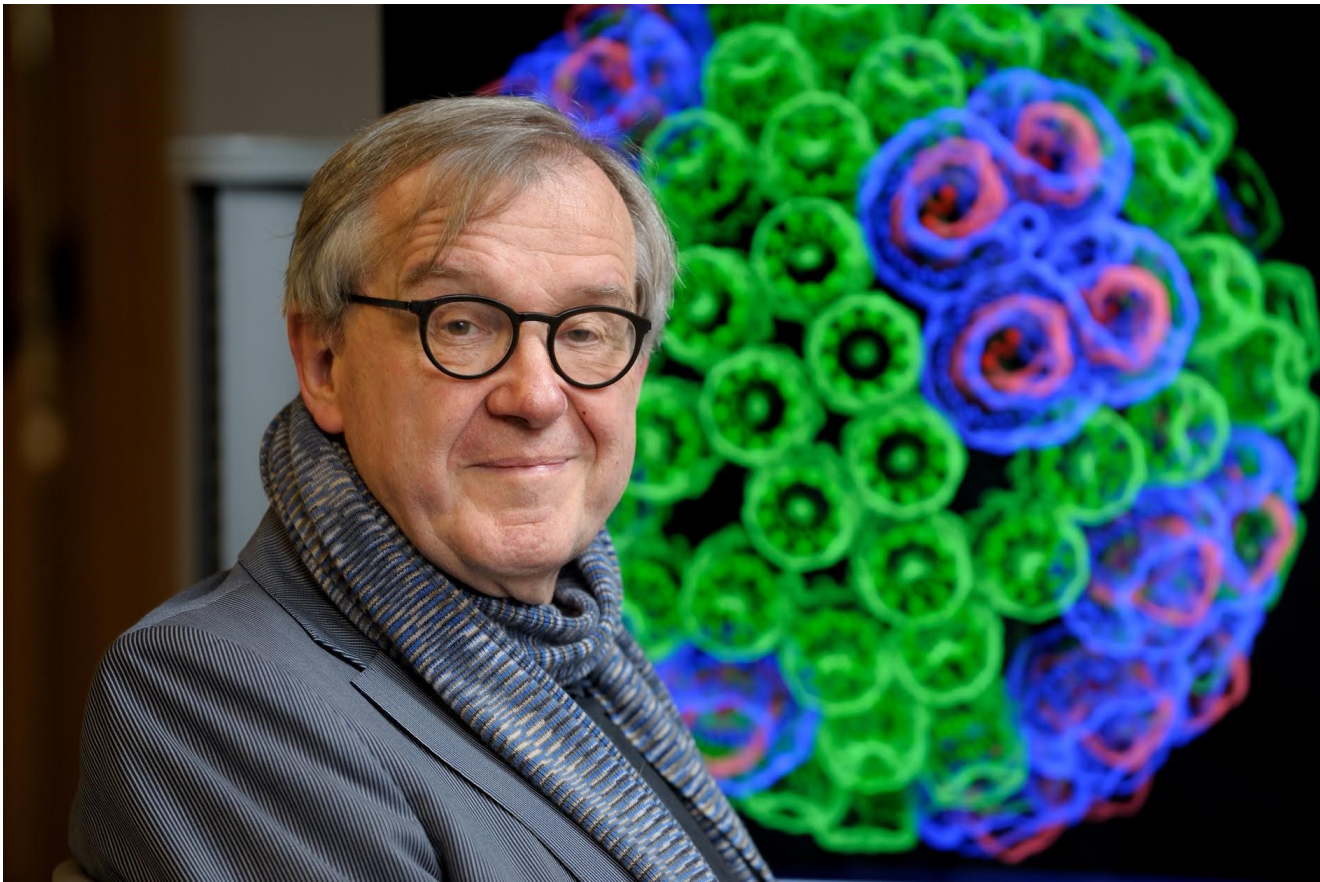
VMD is designed for modeling, visualization, and analysis of biomolecular systems such as proteins, nucleic acids, lipid membranes, carbohydrate structures, etc. VMD provides a wide variety of graphical representations for visualizing and coloring molecular structures: molecular surfaces, space-filling CPK spheres and cylinders, licorice bonds, backbone tubes and ribbons, secondary structure cartoons, and others.

VMD can be used to animate and analyze the trajectory of a molecular dynamics (MD) simulation. In particular, VMD can act as a graphical front end for an external MD program by



# Acknowledgements

- Theoretical and Computational Biophysics Group, University of Illinois at Urbana-Champaign
- NVIDIA CUDA and OptiX teams
- Funding:
  - NIH support: P41GM104601
  - DOE INCITE, ORNL Titan: DE-AC05-00OR22725
  - NSF Blue Waters:  
NSF OCI 07-25070, PRAC “The Computational Microscope”,  
ACI-1238993, ACI-1440026



*“When I was a young man, my goal was to look with mathematical and computational means at the inside of cells, one atom at a time, to decipher how living systems work. That is what I strived for and I never deflected from this goal.” – Klaus Schulten*

# Related Publications

<http://www.ks.uiuc.edu/Research/gpu/>

- **NAMD goes quantum: An integrative suite for hybrid simulations.** Melo, M. C. R.; Bernardi, R. C.; Rudack T.; Scheurer, M.; Riplinger, C.; Phillips, J. C.; Maia, J. D. C.; Rocha, G. D.; Ribeiro, J. V.; Stone, J. E.; Neese, F.; Schulten, K.; Luthey-Schulten, Z.; Nature Methods, 2018. (In press)
- **Challenges of Integrating Stochastic Dynamics and Cryo-electron Tomograms in Whole-cell Simulations.** T. M. Earnest, R. Watanabe, J. E. Stone, J. Mahamid, W. Baumeister, E. Villa, and Z. Luthey-Schulten. J. Physical Chemistry B, 121(15): 3871-3881, 2017.
- **Early Experiences Porting the NAMD and VMD Molecular Simulation and Analysis Software to GPU-Accelerated OpenPOWER Platforms.** J. E. Stone, A.-P. Hynninen, J. C. Phillips, and K. Schulten. International Workshop on OpenPOWER for HPC (IWOPH'16), LNCS 9945, pp. 188-206, 2016.
- **Immersive Molecular Visualization with Omnidirectional Stereoscopic Ray Tracing and Remote Rendering.** J. E. Stone, W. R. Sherman, and K. Schulten. High Performance Data Analysis and Visualization Workshop, IEEE International Parallel and Distributed Processing Symposium Workshop (IPDPSW), pp. 1048-1057, 2016.
- **High Performance Molecular Visualization: In-Situ and Parallel Rendering with EGL.** J. E. Stone, P. Messmer, R. Sisneros, and K. Schulten. High Performance Data Analysis and Visualization Workshop, IEEE International Parallel and Distributed Processing Symposium Workshop (IPDPSW), pp. 1014-1023, 2016.
- **Evaluation of Emerging Energy-Efficient Heterogeneous Computing Platforms for Biomolecular and Cellular Simulation Workloads.** J. E. Stone, M. J. Hallock, J. C. Phillips, J. R. Peterson, Z. Luthey-Schulten, and K. Schulten. 25th International Heterogeneity in Computing Workshop, IEEE International Parallel and Distributed Processing Symposium Workshop (IPDPSW), pp. 89-100, 2016.



# Related Publications

<http://www.ks.uiuc.edu/Research/gpu/>

- **Atomic Detail Visualization of Photosynthetic Membranes with GPU-Accelerated Ray Tracing.** J. E. Stone, M. Sener, K. L. Vandivort, A. Barragan, A. Singharoy, I. Teo, J. V. Ribeiro, B. Isralewitz, B. Liu, B.-C. Goh, J. C. Phillips, C. MacGregor-Chatwin, M. P. Johnson, L. F. Kourkoutis, C. Neil Hunter, and K. Schulten. *J. Parallel Computing*, 55:17-27, 2016.
- **Chemical Visualization of Human Pathogens: the Retroviral Capsids.** Juan R. Perilla, Boon Chong Goh, John E. Stone, and Klaus Schulten. *SC'15 Visualization and Data Analytics Showcase*, 2015.
- **Visualization of Energy Conversion Processes in a Light Harvesting Organelle at Atomic Detail.** M. Sener, J. E. Stone, A. Barragan, A. Singharoy, I. Teo, K. L. Vandivort, B. Isralewitz, B. Liu, B. Goh, J. C. Phillips, L. F. Kourkoutis, C. N. Hunter, and K. Schulten. *SC'14 Visualization and Data Analytics Showcase*, 2014.  
\*\*\*Winner of the **SC'14 Visualization and Data Analytics Showcase**
- **Runtime and Architecture Support for Efficient Data Exchange in Multi-Accelerator Applications.** J. Cabezas, I. Gelado, J. E. Stone, N. Navarro, D. B. Kirk, and W. Hwu. *IEEE Transactions on Parallel and Distributed Systems*, 26(5):1405-1418, 2015.
- **Unlocking the Full Potential of the Cray XK7 Accelerator.** M. D. Klein and J. E. Stone. Cray Users Group, Lugano Switzerland, May 2014.
- **GPU-Accelerated Analysis and Visualization of Large Structures Solved by Molecular Dynamics Flexible Fitting.** J. E. Stone, R. McGreevy, B. Isralewitz, and K. Schulten. *Faraday Discussions*, 169:265-283, 2014.
- **Simulation of reaction diffusion processes over biologically relevant size and time scales using multi-GPU workstations.** M. J. Hallock, J. E. Stone, E. Roberts, C. Fry, and Z. Luthey-Schulten. *Journal of Parallel Computing*, 40:86-99, 2014.

# Related Publications

<http://www.ks.uiuc.edu/Research/gpu/>

- **GPU-Accelerated Molecular Visualization on Petascale Supercomputing Platforms.** J. Stone, K. L. Vandivort, and K. Schulten. *UltraVis'13: Proceedings of the 8th International Workshop on Ultrascale Visualization*, pp. 6:1-6:8, 2013.
- **Early Experiences Scaling VMD Molecular Visualization and Analysis Jobs on Blue Waters.** J. Stone, B. Isralewitz, and K. Schulten. In proceedings, *Extreme Scaling Workshop*, 2013.
- **Lattice Microbes: High-performance stochastic simulation method for the reaction-diffusion master equation.** E. Roberts, J. Stone, and Z. Luthey-Schulten. *J. Computational Chemistry* 34 (3), 245-255, 2013.
- **Fast Visualization of Gaussian Density Surfaces for Molecular Dynamics and Particle System Trajectories.** M. Krone, J. Stone, T. Ertl, and K. Schulten. *EuroVis Short Papers*, pp. 67-71, 2012.
- **Immersive Out-of-Core Visualization of Large-Size and Long-Timescale Molecular Dynamics Trajectories.** J. Stone, K. L. Vandivort, and K. Schulten. G. Bebis et al. (Eds.): *7th International Symposium on Visual Computing (ISVC 2011)*, LNCS 6939, pp. 1-12, 2011.
- **Fast Analysis of Molecular Dynamics Trajectories with Graphics Processing Units – Radial Distribution Functions.** B. Levine, J. Stone, and A. Kohlmeyer. *J. Comp. Physics*, 230(9):3556-3569, 2011.

# Related Publications

<http://www.ks.uiuc.edu/Research/gpu/>

- **Quantifying the Impact of GPUs on Performance and Energy Efficiency in HPC Clusters.** J. Enos, C. Steffen, J. Fullop, M. Showerman, G. Shi, K. Esler, V. Kindratenko, J. Stone, J Phillips. *International Conference on Green Computing*, pp. 317-324, 2010.
- **GPU-accelerated molecular modeling coming of age.** J. Stone, D. Hardy, I. Ufimtsev, K. Schulten. *J. Molecular Graphics and Modeling*, 29:116-125, 2010.
- **OpenCL: A Parallel Programming Standard for Heterogeneous Computing.** J. Stone, D. Gohara, G. Shi. *Computing in Science and Engineering*, 12(3):66-73, 2010.
- **An Asymmetric Distributed Shared Memory Model for Heterogeneous Computing Systems.** I. Gelado, J. Stone, J. Cabezas, S. Patel, N. Navarro, W. Hwu. *ASPLOS '10: Proceedings of the 15<sup>th</sup> International Conference on Architectural Support for Programming Languages and Operating Systems*, pp. 347-358, 2010.



# Related Publications

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- **Probing Biomolecular Machines with Graphics Processors.** J. Phillips, J. Stone. *Communications of the ACM*, 52(10):34-41, 2009.
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- **GPU acceleration of cutoff pair potentials for molecular modeling applications.**  
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- **GPU computing.** J. Owens, M. Houston, D. Luebke, S. Green, J. Stone, J. Phillips. *Proceedings of the IEEE*, 96:879-899, 2008.
- **Accelerating molecular modeling applications with graphics processors.** J. Stone, J. Phillips, P. Freddolino, D. Hardy, L. Trabuco, K. Schulten. *J. Comp. Chem.*, 28:2618-2640, 2007.
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